RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/068,956

DATE: 03/19/2002
TIME: 17:50:38

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<110> APPLICANT: Paul Young et al.
<120> TITLE OF INVENTION: PGRP-L Polynucleotides, Polypeptides, and Antibodies
<130> FILE REFERENCE: PF513P1
<140> CURRENT APPLICATION NUMBER: US/10/068,956
<141> CURRENT FILING DATE: 2002-02-11
<150> PRIOR APPLICATION NUMBER: 60/149,715
<151> PRIOR FILING DATE: 1999-08-20
<150> PRIOR APPLICATION NUMBER: PCT/US00/22877
<151> PRIOR FILING DATE: 2000-08-18
<160> NUMBER OF SEQ ID NOS: 18
<170> SOFTWARE: PatentIn version 3.1
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<211> LENGTH: 1200
<212> TYPE: DNA
<213> ORGANISM: human
<400> SEQUENCE: 1

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tgggccaccg ccagctggtg cgcaccgact gccccggcga cgcgctcttc gacctgctgc 240
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cagctcagcc ccagacccag ccagcctgtc ctttccccag ctcctaatac ctctaccttt 540
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<210> SEQ ID NO: 2
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<212> TYPE: PRT
<213> ORGANISM: human
<400> SEQUENCE: 2

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35 40 45
Arg Ala Gly Leu Leu Arg Pro Asp Tyr Ala Leu Leu Gly His Arg Gln
50 55 60
Leu Val Arg Thr Asp Cys Pro Gly Asp Ala Leu Phe Asp Leu Leu Arg
65 70 75 80
Thr Trp Pro His Phe Thr Ala Val Ser Leu Arg Ser Leu His Tyr Thr
85 90 95
Ala Arg Arg Pro Ser Val Tyr Thr Ser Ser Thr Arg Pro Leu Pro Pro
100 105 110
Ala Cys Asn Ser Cys Ala Arg Thr Ala Ser Ala Arg Pro Pro Thr Ser
115 120 125
Arg Arg His Val Tyr Ser Gly Asn Leu Gly Pro Ala Phe Ala Gly His
130 135 140
Ser Ala Gly Asn Ile Pro Asp Pro Val Thr Ser Ala Tyr Ala Ala Ser
145 150 155 160
Ala Gln Pro Gln Thr Gln Pro Ala Cys Pro Phe Pro Ser Ser
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<211> LENGTH: 1876
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gaaaactaag aactcctttg agagaccctt gaagatccag gaggtattat ccctgatgat 1800
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aaaaaaaaaa aaaaaa 1876

<210> SEQ ID NO: 4
<211> LENGTH: 530
<212> TYPE: PRT
<213> ORGANISM: human
<400> SEQUENCE: 4

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20 25 30
Ile Gln Ala Leu Ala Glu Leu Glu Gln Lys Val Pro Val Thr Glu Ala
35 40 45
Ser Ile Thr Ala Ser Ala Trp Ile Leu Ser Ala Lys Asn Ser Ser Thr
50 55 60
His Asn Ser Leu His Gln Arg Leu Leu Leu Lys Ala Pro Ser His Asn
65 70 75 80
Thr Thr Glu Pro Asp Pro His Ser Leu Ser Pro Glu Leu Gln Ala Leu
85 90 95
Ile Ser Glu Val Ala Gln His Asp Val Gln Asn Gly Arg Glu Tyr Gly
100 105 110
Val Val Leu Ala Pro Asp Gly Ser Thr Val Ala Val Lys Pro Leu Leu
115 120 125
Phe Gly Leu Glu Ala Gly Leu Gln Ala His Ser Val Ala Asn Leu Pro
130 135 140
Ser Asp Cys Leu Ala Ile Pro Cys Asp Thr Gly Asp Thr Leu Ala Asn
145 150 155 160
Ile Arg Ala Thr Trp Pro Gly Leu Met Asp Ala Phe Pro Asn Ala Ser
165 170 175
Ser Pro Asp Val Gly Ala Thr Leu Pro Asn Asp Lys Ala Lys Thr Pro
180 185 190
Thr Thr Val Asp Arg Leu Leu Ala Ile Thr Leu Ala Gly Asp Leu Gly
195 200 205
Leu Thr Phe Leu His Arg Ser Gln Thr Trp Ser Pro Pro Gly Leu Gly
210 215 220
Thr Glu Gly Cys Trp Asp Gln Leu Thr Ala Pro Arg Val Phe Thr Leu
225 230 235 240
Leu Asp Pro Gln Ala Ser Arg Leu Thr Met Ala Phe Leu Asn Gly Ala
245 250 255
Leu Asp Gly Ala Leu Leu Gly Asn His Leu Ser Gln Ile Pro Arg Pro
260 265 270
His Pro Pro Leu Ser His Leu Leu Arg Glu Tyr Tyr Gly Ala Gly Val
275 280 285

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146       Asn Gly Asp Pro Val Phe Arg Ser Asn Phe Arg Arg Gln Asn Gly Ala
147           290                 295                 300
148       Ala Leu Thr Ser Ala Pro Thr Leu Ala Gln Gln Val Trp Glu Ala Leu
149       305                 310                 315                 320
150       Val Leu Leu Gln Lys Leu Glu Pro Glu His Leu Gln Leu Gln Asn Ile
151                       325                 330                 335
152       Ser Gln Glu Gln Leu Ala Gln Val Ala Thr Leu Ala Thr Lys Glu Phe
153                   340                 345                 350
154       Thr Glu Ala Phe Leu Gly Cys Pro Ala Ile His Pro Arg Cys Arg Trp
155               355                 360                 365
156       Gly Ala Ala Pro Tyr Arg Gly His Pro Thr Pro Leu Arg Leu Pro Leu
157           370                 375                 380
158       Gly Phe Leu Tyr Val His His Thr Tyr Val Pro Ala Pro Pro Cys Thr
159       385                 390                 395                 400
160       Thr Phe Gln Ser Cys Ala Ala Asp Met Arg Ser Met Gln Arg Phe His
161                       405                 410                 415
162       Gln Asp Val Arg Lys Trp Asp Asp Ile Gly Tyr Ser Phe Val Val Gly
163                   420                 425                 430
164       Ser Asp Gly Tyr Leu Tyr Gln Gly Arg Gly Trp His Trp Val Gly Ala
165               435                 440                 445
166       His Thr Arg Gly Tyr Asn Ser Arg Gly Phe Gly Val Ala Phe Val Gly
167           450                 455                 460
168       Asn Tyr Thr Gly Ser Leu Pro Asn Glu Ala Ala Leu Asn Thr Val Arg
169       465                 470                 475                 480
170       Asp Ala Leu Pro Ser Cys Ala Ile Arg Glu Gly Leu Leu Arg Pro Asp
171                       485                 490                 495
172       Tyr Lys Leu Leu Gly His Arg Gln Leu Val Leu Thr His Cys Pro Gly
173                   500                 505                 510
174       Asn Ala Leu Phe Asn Leu Leu Arg Thr Trp Pro His Phe Thr Glu Val
175               515                 520                 525
176       Glu Asn
177           530
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180 <211> LENGTH: 733
181 <212> TYPE: DNA
182 <213> ORGANISM: human
183 <400> SEQUENCE: 5
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185       aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga    120
186       tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg    180
187       tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg    240
188       aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact    300
189       ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg    360
190       agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc    420
191       catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct    480
192       atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga    540
193       ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg    600
194       acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc    660
195       acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc    720
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196 gactctagag gat 733
198 <210> SEQ ID NO: 6
199 <211> LENGTH: 5
200 <212> TYPE: PRT
201 <213> ORGANISM: human
202 <220> FEATURE:
203 <221> NAME/KEY: MISC_FEATURE
204 <222> LOCATION: (3)..(3)
205 <223> OTHER INFORMATION: Xaa equals any amino acid
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208 1 5
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211 <211> LENGTH: 86
212 <212> TYPE: DNA
213 <213> ORGANISM: human
214 <400> SEQUENCE: 7
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216 cccgaaatat ctgccatctc aattag 86
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219 <211> LENGTH: 27
220 <212> TYPE: DNA
221 <213> ORGANISM: human
222 <400> SEQUENCE: 8
223 gcggcaagct ttttgcaaag cctaggc 27
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226 <211> LENGTH: 271
227 <212> TYPE: DNA
228 <213> ORGANISM: human
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230 ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60
231 aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 120
232 gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180
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234 ttttggaggc ctaggctttt gcaaaaagct t 271
236 <210> SEQ ID NO: 10
237 <211> LENGTH: 32
238 <212> TYPE: DNA
239 <213> ORGANISM: human
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243 <210> SEQ ID NO: 11
244 <211> LENGTH: 31
245 <212> TYPE: DNA
246 <213> ORGANISM: human
247 <400> SEQUENCE: 11
248 gcgaagcttc gcgactcccc ggatccgcct c 31
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251 <211> LENGTH: 12